<110> APPLICANT: Voellmy, Richard
<120> TITLE OF INVENTION: MOLECULAR REGULATORY CIRCUITS TO ACHIEVE
SUSTAINED ACTIVATION OF GENES OF INTEREST BY A SINGLE STRESS
<130> FILE REFERENCE: 870109.409
<140> CURRENT APPLICATION NUMBER: US/10/046,420
<141> CURRENT FILING DATE: 2002-04-19
<150> PRIOR APPLICATION NUMBER: US/09/304,121
<151> PRIOR FILING DATE: 1999-05-03
<160> NUMBER OF SEQ ID NOS: 3
<170> SOFTWARE: FastSEQ for Windows Version 3.0

<210> SEQ ID NO 1
<211> LENGTH: 2156
<212> TYPE: DNA
<213> ORGANISM: Homo sapien
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (161)...(1747)
<400> SEQUENCE: 1

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gcggcggcgc ggcccggaag gctggcgcgg cgacggcgtt agcccggccc tcggcccctc    120
tttgcggccg ctccctccgc ctattccctc cttgctcgag atg gat ctg ccc gtg      175
                                                Met Asp Leu Pro Val
                                                 1               5

ggc ccc ggc gcg gcg ggg ccc agc aac gtc ccg gcc ttc ctg acc aag      223
Gly Pro Gly Ala Ala Gly Pro Ser Asn Val Pro Ala Phe Leu Thr Lys
                 10                  15                  20

ctg tgg acc ctc gtg agc gac ccg gac acc gac gcg ctc atc tgc tgg      271
Leu Trp Thr Leu Val Ser Asp Pro Asp Thr Asp Ala Leu Ile Cys Trp
             25                  30                  35

agc ccg agc ggg aac agc ttc cac gtg ttc gac cag ggc cag ttt gcc      319
Ser Pro Ser Gly Asn Ser Phe His Val Phe Asp Gln Gly Gln Phe Ala
         40                  45                  50

aag gag gtg ctg ccc aag tac ttc aag cac aac aac atg gcc agc ttc      367
Lys Glu Val Leu Pro Lys Tyr Phe Lys His Asn Asn Met Ala Ser Phe
     55                  60                  65

gtg cgg cag ctc aac atg tat ggc ttc cgg aaa gtg gtc cac atc gag      415
Val Arg Gln Leu Asn Met Tyr Gly Phe Arg Lys Val Val His Ile Glu
 70                  75                  80                  85

cag ggc ggc ctg gtc aag cca gag aga gac gac acg gag ttc cag cac      463
Gln Gly Gly Leu Val Lys Pro Glu Arg Asp Asp Thr Glu Phe Gln His
                 90                  95                 100

cca tgc ttc ctg cgt ggc cag gag cag ctc ctt gag aac atc aag agg      511
Pro Cys Phe Leu Arg Gly Gln Glu Gln Leu Leu Glu Asn Ile Lys Arg
             105                 110                 115

aaa gtg acc agt gtg tcc acc ctg aag agt gaa gac ata aag atc cgc      559
Lys Val Thr Ser Val Ser Thr Leu Lys Ser Glu Asp Ile Lys Ile Arg
         120                 125                 130

cag gac agc gtc acc aag ctg ctg acg gac gtg cag ctg atg aag ggg      607
Gln Asp Ser Val Thr Lys Leu Leu Thr Asp Val Gln Leu Met Lys Gly
     135                 140                 145

aag cag gag tgc atg gac tcc aag ctc ctg gcc atg aag cat gag aat      655
Lys Gln Glu Cys Met Asp Ser Lys Leu Leu Ala Met Lys His Glu Asn
150                 155                 160                 165

gag gct ctg tgg cgg gag gtg gcc agc ctt cgg cag aag cat gcc cag      703
Glu Ala Leu Trp Arg Glu Val Ala Ser Leu Arg Gln Lys His Ala Gln
                 170                 175                 180

caa cag aaa gtc gtc aac aag ctc att cag ttc ctg atc tca ctg gtg      751
Gln Gln Lys Val Val Asn Lys Leu Ile Gln Phe Leu Ile Ser Leu Val
             185                 190                 195

cag tca aac cgg atc ctg ggg gtg aag aga aag atc ccc ctg atg ctg      799
Gln Ser Asn Arg Ile Leu Gly Val Lys Arg Lys Ile Pro Leu Met Leu
         200                 205                 210

aac gac agt ggc tca gca cat tcc atg ccc aag tat agc cgg cag ttc      847
Asn Asp Ser Gly Ser Ala His Ser Met Pro Lys Tyr Ser Arg Gln Phe
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    215                 220                 225
tcc ctg gag cac gtc cac ggc tcg ggc ccc tac tcg gcc ccc tcc cca      895
Ser Leu Glu His Val His Gly Ser Gly Pro Tyr Ser Ala Pro Ser Pro
230                 235                 240                 245
gcc tac agc agc tcc agc ctc tac gcc cct gat gct gtg gcc agc tct      943
Ala Tyr Ser Ser Ser Ser Leu Tyr Ala Pro Asp Ala Val Ala Ser Ser
                250                 255                 260
gga ccc atc atc tcc gac atc acc gag ctg gct cct gcc agc ccc atg      991
Gly Pro Ile Ile Ser Asp Ile Thr Glu Leu Ala Pro Ala Ser Pro Met
            265                 270                 275
gcc tcc ccc ggc ggg agc ata gac gag agg ccc cta tcc agc agc ccc     1039
Ala Ser Pro Gly Gly Ser Ile Asp Glu Arg Pro Leu Ser Ser Ser Pro
        280                 285                 290
ctg gtg cgt gtc aag gag gag ccc ccc agc ccg cct cag agc ccc cgg     1087
Leu Val Arg Val Lys Glu Glu Pro Pro Ser Pro Pro Gln Ser Pro Arg
    295                 300                 305
gta gag gag gcg agt ccc ggg cgc cca tct tcc gtg gac acc ctc ttg     1135
Val Glu Glu Ala Ser Pro Gly Arg Pro Ser Ser Val Asp Thr Leu Leu
310                 315                 320                 325
tcc ccg acc gcc ctc att gac tcc atc ctg cgg gag agt gaa cct gcc     1183
Ser Pro Thr Ala Leu Ile Asp Ser Ile Leu Arg Glu Ser Glu Pro Ala
                330                 335                 340
ccc gcc tcc gtc aca gcc ctc acg gac gcc agg ggc cac acg gac acc     1231
Pro Ala Ser Val Thr Ala Leu Thr Asp Ala Arg Gly His Thr Asp Thr
            345                 350                 355
gag ggc cgg cct ccc tcc ccc ccg ccc acc tcc acc cct gaa aag tgc     1279
Glu Gly Arg Pro Pro Ser Pro Pro Pro Thr Ser Thr Pro Glu Lys Cys
        360                 365                 370
ctc agc gta gcc tgc ctg gac aag aat gag ctc agt gac cac ttg gat     1327
Leu Ser Val Ala Cys Leu Asp Lys Asn Glu Leu Ser Asp His Leu Asp
    375                 380                 385
gct atg gac tcc aac ctg gat aac ctg cag acc atg ctg agc agc cac     1375
Ala Met Asp Ser Asn Leu Asp Asn Leu Gln Thr Met Leu Ser Ser His
390                 395                 400                 405
ggc ttc agc gtg gac acc agt gcc ctg ctg gac ctg ttc agc ccc tcg     1423
Gly Phe Ser Val Asp Thr Ser Ala Leu Leu Asp Leu Phe Ser Pro Ser
                410                 415                 420
gtg acc gtg ccc gac atg agc ctg cct gac ctt gac agc agc ctg gcc     1471
Val Thr Val Pro Asp Met Ser Leu Pro Asp Leu Asp Ser Ser Leu Ala
            425                 430                 435
agt atc caa gag ctc ctg tct ccc cag gag ccc ccc agg cct ccc gag     1519
Ser Ile Gln Glu Leu Leu Ser Pro Gln Glu Pro Pro Arg Pro Pro Glu
        440                 445                 450
gca gag aac agc agc ccg gat tca ggg aag cag ctg gtg cac tac aca     1567
Ala Glu Asn Ser Ser Pro Asp Ser Gly Lys Gln Leu Val His Tyr Thr
    455                 460                 465
gcg cag ccg ctg ttc ctg ctg gac ccc ggc tcc gtg gac acc ggg agc     1615
Ala Gln Pro Leu Phe Leu Leu Asp Pro Gly Ser Val Asp Thr Gly Ser
470                 475                 480                 485
aac gac ctg ccg gtg ctg ttt gag ctg gga gag ggc tcc tac ttc tcc     1663
Asn Asp Leu Pro Val Leu Phe Glu Leu Gly Glu Gly Ser Tyr Phe Ser
                490                 495                 500
gaa ggg gac ggc ttc gcc gag gac ccc acc atc tcc ctg ctg aca ggc     1711
Glu Gly Asp Gly Phe Ala Glu Asp Pro Thr Ile Ser Leu Leu Thr Gly
            505                 510                 515
tcg gag cct ccc aaa gcc aag gac ccc act gtc tcc tagaggcccc          1757
Ser Glu Pro Pro Lys Ala Lys Asp Pro Thr Val Ser
        520                 525
ggaggagctg ggccagccgc ccacccccac ccccagtgca gggctggtct tggggaggca   1817
gggcagcctc gcggtcttgg gcactggtgg gtcggccgcc atagccccag taggacaaac   1877
gggctcgggt ctgggcagca cctctggtca ggagggtcac cctggcctgc cagtctgcct   1937
tcccccaacc ccgtgtcctg tggtttggtt ggggcttcac agccacacct ggactgaccc   1997
tgcaggttgt tcatagtcag aattgtattt tggattttta cacaactgtc ccgttccccg   2057
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ctataaacag acaggctcta aaaaaaaaaa aaaaaaaaa                          2156
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<210> SEQ ID NO 2
<211> LENGTH: 529
<212> TYPE: PRT
<213> ORGANISM: Homo sapien
<400> SEQUENCE: 2

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Ala Phe Leu Thr Lys Leu Trp Thr Leu Val Ser Asp Pro Asp Thr Asp
            20                  25                  30
Ala Leu Ile Cys Trp Ser Pro Ser Gly Asn Ser Phe His Val Phe Asp
        35                  40                  45
Gln Gly Gln Phe Ala Lys Glu Val Leu Pro Lys Tyr Phe Lys His Asn
    50                  55                  60
Asn Met Ala Ser Phe Val Arg Gln Leu Asn Met Tyr Gly Phe Arg Lys
65                  70                  75                  80
Val Val His Ile Glu Gln Gly Gly Leu Val Lys Pro Glu Arg Asp Asp
                85                  90                  95
Thr Glu Phe Gln His Pro Cys Phe Leu Arg Gly Gln Glu Gln Leu Leu
            100                 105                 110
Glu Asn Ile Lys Arg Lys Val Thr Ser Val Ser Thr Leu Lys Ser Glu
        115                 120                 125
Asp Ile Lys Ile Arg Gln Asp Ser Val Thr Lys Leu Leu Thr Asp Val
    130                 135                 140
Gln Leu Met Lys Gly Lys Gln Glu Cys Met Asp Ser Lys Leu Leu Ala
145                 150                 155                 160
Met Lys His Glu Asn Glu Ala Leu Trp Arg Glu Val Ala Ser Leu Arg
                165                 170                 175
Gln Lys His Ala Gln Gln Gln Lys Val Val Asn Lys Leu Ile Gln Phe
            180                 185                 190
Leu Ile Ser Leu Val Gln Ser Asn Arg Ile Leu Gly Val Lys Arg Lys
        195                 200                 205
Ile Pro Leu Met Leu Asn Asp Ser Gly Ser Ala His Ser Met Pro Lys
    210                 215                 220
Tyr Ser Arg Gln Phe Ser Leu Glu His Val His Gly Ser Gly Pro Tyr
225                 230                 235                 240
Ser Ala Pro Ser Pro Ala Tyr Ser Ser Ser Ser Leu Tyr Ala Pro Asp
                245                 250                 255
Ala Val Ala Ser Ser Gly Pro Ile Ile Ser Asp Ile Thr Glu Leu Ala
            260                 265                 270
Pro Ala Ser Pro Met Ala Ser Pro Gly Gly Ser Ile Asp Glu Arg Pro
        275                 280                 285
Leu Ser Ser Ser Pro Leu Val Arg Val Lys Glu Glu Pro Pro Ser Pro
    290                 295                 300
Pro Gln Ser Pro Arg Val Glu Glu Ala Ser Pro Gly Arg Pro Ser Ser
305                 310                 315                 320
Val Asp Thr Leu Leu Ser Pro Thr Ala Leu Ile Asp Ser Ile Leu Arg
                325                 330                 335
Glu Ser Glu Pro Ala Pro Ala Ser Val Thr Ala Leu Thr Asp Ala Arg
            340                 345                 350
Gly His Thr Asp Thr Glu Gly Arg Pro Pro Ser Pro Pro Pro Thr Ser
        355                 360                 365
Thr Pro Glu Lys Cys Leu Ser Val Ala Cys Leu Asp Lys Asn Glu Leu
    370                 375                 380
Ser Asp His Leu Asp Ala Met Asp Ser Asn Leu Asp Asn Leu Gln Thr
385                 390                 395                 400
Met Leu Ser Ser His Gly Phe Ser Val Asp Thr Ser Ala Leu Leu Asp
                405                 410                 415
Leu Phe Ser Pro Ser Val Thr Val Pro Asp Met Ser Leu Pro Asp Leu
            420                 425                 430
Asp Ser Ser Leu Ala Ser Ile Gln Glu Leu Leu Ser Pro Gln Glu Pro
        435                 440                 445
Pro Arg Pro Pro Glu Ala Glu Asn Ser Ser Pro Asp Ser Gly Lys Gln
    450                 455                 460
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      Leu Val His Tyr Thr Ala Gln Pro Leu Phe Leu Leu Asp Pro Gly Ser
      465                 470                 475                 480
      Val Asp Thr Gly Ser Asn Asp Leu Pro Val Leu Phe Glu Leu Gly Glu
                      485                 490                 495
      Gly Ser Tyr Phe Ser Glu Gly Asp Gly Phe Ala Glu Asp Pro Thr Ile
                  500                 505                 510
      Ser Leu Leu Thr Gly Ser Glu Pro Pro Lys Ala Lys Asp Pro Thr Val
              515                 520                 525
      Ser

<210> SEQ ID NO 3
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: A heat shock element.  A nucleic acid molecule
      that binds with a heat shock transcription factor
      to stimulate gene expression
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)...(25)
<223> OTHER INFORMATION: n = A,T,C or G
<400> SEQUENCE: 3
      ngaannttcn nnnnnnttcn ngaan                                          25
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